- 1 -

## SEQUENCE LISTING

<110>	Hepgenics Pty Ltd	
<120>	Viral Vector	
<130>	12437050/EJH	
<150>	AU 2003901876	
<151>	2003-04-17	
<160>	13	
<170>	PatentIn version 3.0	
<210>	1	
<211>	25	
<212>	DNA	
<213>	duck	
	,	
<400>	1 catc cagcaaaatc aatgg	25
gggcaa	care cageaaaare aaryg	25
<210>	2	
<211>	30	
<212>	DNA	
<213>	human	

<400> 2

gctgcggaat ggctaaaagg gcccccgacc

30

- 2 -

<210>	3						
<211>	34						
<212>	DNA						
<213>	huma	an					
<400>	3 ctao	atcacgaaac	ccacgtcacc	aaaa			34
				9999			24
<210>	4						
<211>	34						
<212>	DNA						
<213>	huma	an					
<400>	4 ratc	tagtgctttg	ggtgcagtgg	cccc			34
	,		, 93-9-49-99				24
<210>	5						
<211>	3021	l					
<212>	DNA						
<213>	duc	c					
<400> catgcto	_	tgaaagctta	tgcaaaaatt	aacgaggaat	cactggatag	ggctaggaga	60
ttgcttt	ggt	ggcattacaa	ctgtttactg	tggggagaag	ctcaagttac	taactatatt	120
tctcgtt	tgc	gtacttggtt	gtcaactcct	gagaaatata	gaggtagaga	tgccccgacc	180
attgaag	caa	tcactagacc	aatccaggtg	gctcagggag	gcagaaaaac	aactacgggt	240
actagaa	aac	ctcgtggact	cgaacctaga	agaagaaaag	ttaaaaccac	agttgtctat	300
gggagaa	gac	gttcaaagtc	ccgggaaagg	agagccccta	caccccaacg	tgcgggctcc	360
cctctcc	cac	gtagttcgag	cagccaccat	agatctccct	cgcctaggaa	ataaattacc	420
tgctagg	cat	cacttaggta	aattgtcagg	actatatcaa	atgaagggct	gtacttttaa	480
cccagaa	tgg	aaagtaccag	atatttcgga	tactcatttt	aatttagatg	tagttaatga	540

gtgcccttcc cgaaattgga aatatttgac tccagccaaa ttctggccca agagcatttc 600 ctactttcct gtccaggtag gggttaaacc aaagtatcct gacaatgtga tgcaacatga 660 atcaatagta ggtaaatatt taaccagget ctatgaagca ggaateettt ataageggat 720 atctaaacat ttggtcacat ttaaaggtca gccttataat tgggaacagc aacaccttgt 780 caatcaacat cacatttatg atggggcaac atccagcaaa atcaatggac gtcagacgga 840 tagaaggagg agaaatactg ttaaaccaac ttgccggaag gatgatccca aaagggactt 900 tgacatggtc aggcaagttt ccaacactag atcacgtgtt agaccatgtg caaacaatgg 960 aggagataaa caccctccag aatcagggag cttggcctgc tggggcggga aggagagtag 1020 gattatcaaa toogactoot caagagatto otcagoocca gtggactooc gaggaagaco 1080 aaaaagcacg cgaagctttt cgccgttatc aagaagaaag accaccggaa accaccacca 1140 ttoctccgtc ttcccctcct cagtggaagc tacaacccgg ggacgatcca ctcctgggaa 1200 atcagtctct cctcgagact catccgctat accagtcaga accagcggtg ccagtgataa 1260 aaactccccc cttgaagaag aaaatgtctg gtaccttcgg gggaatacta gctggcctaa 1320 toggattact ggtaagottt ttottgttga taaaaattot agaaatactg aggaggotag 1380 attggtggtg gatttctctc agttctccaa agggaaaaaat gcaatgcgct ttccaagata 1440 ctggagccca aatctctcca cattacgtag gatcttgccc gtggggatgc ccaggatttc 1500 tttggaccta tctcaggctt tttatcatct tcctcttaat cctgctagta gcagcaggct 1560 tgctgtatct gacggacaac gggtctacta ttttaggaaa gctccaatgg gcgtcggtct 1620 cagccetttt etectecate tetteactae tgeeetegga teegaaatet etegtegett 1680 taacgtttgg actttcactt atatggatga cttcctcctc tgccacccaa acgctcgtca 1740 ccttaacgca attagccacg ctgtctgctc ttttttacaa gagttaggaa taagaataaa 1800 ctttgacaaa accacgcctt ctccggtgaa tgaaataaga ttcctcggtt accagattga 1860 tgaaaatttc atgaagattg aagaaagcag atggaaagaa ttaaggactg taatcaagaa 1920 aataaaagta ggagaatggt atgactggaa atgtattcaa agatttgtgg ggcatttgaa 1980 ttttgttttg ccttttacta aaggtaatat tgaaatgtta aaaccaatgt atgctgctat 2040 tactaaccaa gtaaacttta gcttctcttc atcctatagg actttgttat ataaactaac 2100 aatgggtgtg tgtaaattaa gaataaagcc aaagtcctct gtacctttgc cacgtgtagc 2160 tacagatgct accccaacac atggcgcaat atcccatatc accggcggga gcgcagtgtt 2220

-4-

tgctttttca	aaggtcagag	atatacatgt	tcaggaacta	ttgatgtctt	gtttagccaa	2280
gataatgatt	aaaccacgtt	gtctcttatc	tgattcaact	tttgtttgcc	ataagcgtta	2340
tcagacgtta	ccatggcatt	ttgctatgtt	ggccaaacaa	ttgctcaaac	cgatacaatt	2400
gtactttgtc	ccgagcaaat	ataatcctgc	tgacggccca	tccaggcaca	aacctcctga	2460
ttggacggct	tttccataca	cccctctctc	gaaagcaata	tatattccac	ataggctatg	2520
tggaacttaa	gaattacacc	cctctccttc	ggagctgctt	gccaaggtat	ctttacgtct	2580
acattgctgt	tgtcgtgtgt	gactgtacct	ttggtatgta	ccattgttta	tgattcttgc	2640
ttatatatgg	atatcaatgc	ttctagagcc	ttagccaatg	tgtatgatct	accagatgat	2700
ttctttccaa	aaatagatga	tcttgttaga	gatgctaaag	acgctttaga	gccttattgg	2760
aaatcagatt	caataaagaa	acatgttttg	attgcaactc	actttgtgga	tctcattgaa	2820
gacttctggc	agactacaca	gggcatgcat	gaaatagccg	aatcattaag	agctgttata	2880
cctcccacta	ctactcctgt	tccaccgggt	tatcttattc	agcacgagga	agctgaagag	2940
atacctttgg	gagatttatt	taaacaccaa	gaagaaagga	tagtaagttt	ccaacccgac	3000
tatccgatta	cggctagaat	t				3021

<210> 6

<211> 984

<212> DNA

<213> duck

<220>

<221> CDS

<222> (1)..(984)

<400> 6 atg ggg caa cat cca gca aaa tca atg gac gtc aga cgg ata gaa gga 48 Met Gly Gln His Pro Ala Lys Ser Met Asp Val Arg Arg Ile Glu Gly gga gaa ata ctg tta aac caa ctt gcc gga agg atg atc cca aaa ggg 96 Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly 20 act ttg aca tgg tca ggc aag ttt cca aca cta gat cac gtg tta gac 144

- 5 -

Thr	Leu	Thr 35	Trp	Ser	Gly	Lys	Phe 40	Pro	Thr	Leu	Asp	His 45	Val	Leu	Asp	•
cat His	gtg Val 50	caa Gln	aca Thr	atg Met	gag Glu	gag Glu 55	ata Ile	aac Asn	acc Thr	ctc Leu	cag Gln 60	aat Asn	cag Glņ	gga Gly	gct Ala	192
tgg Trp 65	cct Pro	gct Ala	Gly ggg	gcg Ala	gga Gly 70	agg Arg	aga Arg	gta Val	gga Gly	tta Leu 75	tca Ser	aat Asn	ccg Pro	act Thr	cct Pro 80	240
caa Gln	gag Glu	att Ile	cct Pro	cag Gln 85	ccc Pro	cag Gln	tgg Trp	act Thr	ccc Pro 90	gag Glu	gaa Glu	gac Asp	caa Gln	aaa Lys 95	gca Ala	288
cgc Arg	gaa Glu	gct Ala	ttt Phe 100	cgc Arg	cgt Arg	tat Tyr	caa Gln	gaa Glu 105	gaa Glu	aga Arg	cca Pro	ccg Pro	gaa Glu 110	acc Thr	acc Thr	336
acc Thr	att Ile	cct Pro 115	ccg Pro	tct Ser	tcc Ser	cct Pro	cct Pro 120	cag Gln	tgg Trp	aag Lys	cta Leu	caa Gln 125	ccc Pro	ggg Gly	gac Asp	384
gat Asp	cca Pro 130	ctc Leu	ctg Leu	gga Gly	aat Asn	cag Gln 135	tct Ser	ctc Leu	ctc Leu	gag Glu	act Thr 140	cat His	ccg Pro	cta Leu	tac Tyr	432
cag Gln 145	Ser	gaa Glu	cca Pro	gcg Ala	gtg Val 150	cca Pro	gtg Val	ata Ile	aaa Lys	act Thr 155	ccc Pro	ccc Pro	ttg Leu	aag Lys	aag Lys 160	480
aaa Lys	atg Met	tct Ser	ggt Gly	acc Thr 165	ttc Phe	Gly ggg	gga Gly	ata Ile	cta Leu 170	gct Ala	ggc	cta Leu	atc Ile	gga Gly 175	tta Leu	528
ctg Leu	gta Val	agc Ser	ttt Phe 180	Phe	ttg Leu	ttg Leu	ata Ile	aaa Lys 185	Ile	cta Leu	gaa Glu	ata Ile	ctg Leu 190	agg Arg	agg Arg	576
cta Leu	gat Asp	tgg Trp 195	Trp	tgg Trp	att Ile	tct Ser	ctc Leu 200	agt Ser	tct Ser	cca Pro	aag Lys	gga Gly 205	Lys	atg Met	caa Gln	624
tgc Cys	gct Ala 210	Phe	caa Gln	gat Asp	act Thr	gga Gly 215	Ala	caa Gln	atc Ile	tct Ser	cca Pro 220	His	tac Tyr	gta Val	gga Gly	672
tct Ser 225	Cys	ccg	tgg Trp	gga Gly	tgc Cys 230	Pro	gga Gly	ttt Phe	ctt Leu	tgg Trp 235	Thr	tat Tyr	ctc Leu	agg Arg	ctt Leu 240	720
ttt Phe	ato lle	ato Ile	ttc Phe	ctc Leu 245	Leu	ato Ile	ctg Leu	cta Leu	gta Val 250	Ala	gca Ala	ggc	ttg Leu	ctg Leu 255	tat Tyr	768
ctç Lev	acc Thr	gac Asp	aac Asn	Gly	tct Ser	act Thr	att	tta Leu	gga Gly	aag Lys	cto Leu	caa Gln	tgg Trp	gcg Ala	tcg Ser	816

-6-

			260					265					270			
gtc Val	tca Ser	gcc Ala 275	ctt Leù	ttc Phe	tcc Ser	tcc Ser	atc Ile 280	tct Ser	tca Ser	cta Leu	ctg Leu	ccc Pro 285	tcg Ser	gat Asp	ccg Pro	864
aaa Lys	tct Ser 290	ctc Leu	gtc Val	gct Ala	tta Leu	acg Thr 295	ttt Phe	gga Gly	ctt Leu	tca Ser	ctt Leu 300	ata Ile	tgg Trp	atg Met	act Thr	912
tcc Ser 305	tcc Ser	tct Ser	gcc Ala	acc Thr	caa Gln 310	acg Thr	ctc Leu	gtc Val	acc Thr	tta Leu 315	acg Thr	caa Gln	tta Leu	gcc Ala	acg Thr 320	960
						aag Lys										984
<210	)> '	7														
<211		328														
<212	?> ]	PRT														
<213	3> c	duck														
<400	)> 7	7														
Met 1	Gly	Gln	His	Pro 5	Ala	Lys	Ser	Met	Asp 10	Val	Arg	Arg	Ile	Glu 15	Gly	
Gly	Glu	Ile	Leu 20	Leu	Asn	Gln	Leu	Ala 25	Gly	Arg	Met	Ile	Pro 30	Lys	Gly	
Thr	Leu	Thr 35	Trp	Ser	Gly	Lys	Phe 40	Pro	Thr	Leu	Asp	His 45	Val	Leu	Asp	
His	Val 50	Gln	Thr	Met	Glu	Glu 55	Ile	Asn	Thr	Leu	Gln 60	Asn	Gln	Gly	Ala	
Trp 65	Pro	Ala	Gly	Ala	Gly 70	Arg	Arg	Val	Gly	Leu 75	Ser	Asn	Pro	Thr	Pro 80	
Gln	Glu	Ile	Pro	Gln 85	Pro	Gln	Trp	Thr	Pro 90	Glu	Glu	Asp	Gln	Lys 95	Ala	

Thr	Ile	Pro 115	Pro	Ser	Ser	Pro	Pro 120	Gln	Trp	Lys	Leu	Gln 125	Pro	Gly	Asp
Asp	Pro 130	Leu	Leu	Gly	Asn	Gln 135	Ser	Leu	Leu	Glu	Thr 140	His	Pro	Leu	Tyr
Gln 145	Ser	Glu	Pro	Ala	Val 150	Pro	Val	Ile	Lys	Thr 155	Pro	Pro	Leu	Lys	Lys 160
Lys	Met	Ser	Gly	Thr 165	Phe	Gly	Gly	Ile	Leu 170	Ala	Gly	Leu	Ile	Gly 175	Leu
Leu	Val	Ser	Phe 180	Phe	Leu	Leu	Ile	Lys 185	Ile	Leu	Glu	Ile	Leu 190	Arg	Arg
Leu	Asp	Trp 195	Trp	Trp	Ile	Ser	Leu 200	Ser	Ser	Pro	Lys	Gly 205	Lys	Met	Gln
Суѕ	Ala 210	Phe	Gln	Asp	Thr	Gly 215	Ala	Gln	Ile	Ser	Pro 220	His	Tyr	Val	Gly
Ser 225	Cys	Pro	Trp	Gly	Cys 230	Pro	Gly	Phe	Leu	Trp 235	Thr	Tyr	Leu	Arg	Leu 240
Phe	Ile	Ile	Phe	Leu 245	Leu	Ile	Leu	Leu	Val 250	Ala	Ala	Gly	Leu	Leu 255	Tyr
Leu	Thr	Asp	Asn 260	Gly	Ser	Thr	Ile	Leu 265	Gly	Lys	Leu	Gln	Trp 270	Ala	Ser
Val	Ser	Ala 275	Leu	Phe	Ser	Ser	Ile 280	Ser	Ser	Leu	Leu	Pro 285	Ser	Asp	Pro
Lys	Ser 290	Leu	Val	Ala	Leu	Thr 295	Phe	Gly	Leu	Ser	Leu 300	Ile	Trp	Met	Thr
Ser 305	Ser	Ser	Ala	Thr	Gln 310	Thr	Leu	Val	Thr	Leu 315	Thr	Gln	Leu	Ala	Thr 320
T	0	7.1 -	T a	Dh-	m	T	00=								

Leu Ser Ala Leu Phe Tyr Lys Ser 325

- 8 -

<210> <211> 501 <212> DNA <213> duck <220> <221> CDS (1)..(501) <222> <400> 8 48 atg tct ggt acc ttc ggg gga ata cta gct ggc cta atc gga tta ctg Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu Leu 96 gta agc ttt ttc ttg ttg ata aaa att cta gaa ata ctg agg agg cta Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg Leu 144 gat tgg tgg att tct ctc agt tct cca aag gga aaa atg caa tgc Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln Cys 40 192 get tte caa gat act gga gee caa ate tet eea cat tae gta gga tet Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly Ser 50. tgc ccg tgg gga tgc cca gga ttt ctt tgg acc tat ctc agg ctt ttt 240 Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu Phe 65 288 atc atc ttc ctc tta atc ctg cta gta gca gcc ttg ctg tat ctg Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr Leu 90 85 336 acq gac aac ggg tct act att tta gga aag ctc caa tgg gcg tcg gtc Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser Val 105 100 tca gcc ctt ttc tcc tcc atc tct tca cta ctg ccc tcg gat ccg aaa 384 Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro Lys 125 115 120 tct ctc gtc gct tta acg ttt gga ctt tca ctt ata tgg atg act tcc 432 Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr Ser 140 130 135 480 tee tet que ace caa acq etc gte ace tta acq caa tta gee acq etg

-9-

Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr Leu 145 150 155 160

tct gct ctt ttt tac aag agt Ser Ala Leu Phe Tyr Lys Ser 165 501

<210> 9

<211> 167

<212> PRT

<213> duck

<400> 9

Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu Leu 1 5 10 15

Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg Leu 20 25 30

Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln Cys 35 40 45

Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly Ser 50 55 60

Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu Phe 65 70 75 80

Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr Leu 85 90 95

Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser Val 100 105 110

Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro Lys 115 120 125

Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr Ser 130 135 140

Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr Leu

- 10 -

145	150	155	160
Ser Ala Leu Phe Tyr 165			
<210> 10	·		
<211> 483			
<212> DNA			
<213> duck		•	
<220>			
<221> CDS	·		
<222> (1)(483)			
<400> 10 atg ggg caa cat cc Met Gly Gln His Pr 1 5	ca gca aaa tca atg ga co Ala Lys Ser Met As 10	sp Val Arg Arg Ile	gaa gga 48 Glu Gly 15
gga gaa ata ctg tt Gly Glu Ile Leu Le 20	ca aac caa ctt gcc go eu Asn Gln Leu Ala Gi 25	ga agg atg atc cca ly Arg Met Ile Pro 30	aaa ggg 96 Lys Gly
act ttg aca tgg to Thr Leu Thr Trp Se 35	ca ggc aag ttt cca acer Gly Lys Phe Pro Th 40	ca cta gat cac gtg hr Leu Asp His Val 45	tta gac 144 Lieu Asp
cat gtg caa aca at His Val Gln Thr Me 50	tg gag gag ata aac ac et Glu Glu Ile Asn Ti 55	hr Leu Gln Asn Gln	gga gct 192 Gly Ala
tgg cct gct ggg go Trp Pro Ala Gly Al 65	cg gga agg aga gta g la Gly Arg Arg Val G 70	ga tta tca aat ccg ly Leu Ser Asn Pro 75	act cct 240 Thr Pro 80
caa gag att cct ca Gln Glu Ile Pro G 89	ag ccc cag tgg act c ln Pro Gln Trp Thr P 5 9	ro Glu Glu Asp Gln	aaa gca 288 Lys Ala 95
cgc gaa gct ttt c Arg Glu Ala Phe A: 100	gc cgt tat caa gaa g rg Arg Tyr Gln Glu G 105	aa aga cca ccg gaa lu Arg Pro Pro Glu 110	acc acc 336 Thr Thr
acc att cct ccg to Thr Ile Pro Pro So 115	ct tcc cct cct cag t er Ser Pro Pro Gln T 120	gg aag cta caa ccc rp Lys Leu Gln Pro 125	ggg gac 384 Gly Asp

- 11 -

Asp		ctc Leu														432
		gaa Glu														480
aaa Lys																483
<210	)>	11														
<211	.>	161														
<212	!>	PRT														
<213	3>	duck														
<400	)>	11														
Met 1	Gly	Gln	His	Pro 5	Ala	Lys	Ser	Met	Asp 10	Val	Arg	Arg	Ile	Glu 15	Gly	
Gly	Glu	Ile	Leu 20	Leu	Asn	Gln	Leu	Ala 25	Gly	Arg	Met	Ile	Pro 30	Lys	Gly	
Thr	Leu	Thr 35	Trp	Ser	Gly	Lys	Phe 40	Pro	Thr	Leu	Asp	His 45	Val	Leu	Asp	
His	Val 50	Gln	Thr	Met	Glu	Glu 55	Ile	Asn	Thr	Leu	Gln 60	Asn	Gln	Gly	Ala	
Trp 65	Pro	Ala	Gly	Ala	Gly 70	Arg	Arg	Val	Gly	Leu 75	Ser	Asn	Pro	Thr	Pro 80	
Gln	Glu	Ile	Pro	Gln 85	Pro	Gln	Trp	Thr	Pro 90	Glu	Glu	Asp	Gln	Lys 95	Ala	
Arg	Glu	Ala	Phe 100	Arg	Arg	Tyr	Gln	Glu 105	Glu	Arg	Pro	Pro	Glu 110	Thr	Thr	
Thr	Ile	Pro 115	Pro	Ser	Ser	Pro	Pro 120	Gln	Trp	Lys	Leu	Gln 125	Pro	Gly	Asp	

- 12 -

130	u Leu	Gly	Asn	Gln 135	Ser	Leu	Leu	Glu	Thr 140	His	Pro	Leu	Tyr	
Gln Ser Gl 145	u Pro	Ala	Val 150	Pro	Val	Ile	Lys	Thr 155	Pro	Pro	Leu	Lys	Lys 160	
Lys														
<210> 12														
<211> 501														
<212> DNA	1													
<213> du	:k													
<220>											<b>.</b>			
<221> CDS	3													
<222> (1)	(50	L)												
<400> 12		***	~~~			at a	~~+	~~~	a+ a	2+2	~~~	<b>+</b> + •	a+-	4.9
<400> 12 atg tct gg Met Ser G														48
atg tct go Met Ser G	y Thr	Phe 5 ttg	Gly	Gly	Ile aaa	Leu att	Ala 10 cta	Gly gaa	Leu	<pre>Ile ctg</pre>	Gly agg	Leu 15 agg	Leu cta	48 96
atg tct gg Met Ser Gi 1 gta agc tt Val Ser Pl gat tgg tg Asp Trp Ti	t ttc e Phe 20 gg tgg	Phe 5 ttg Leu att	ttg Leu tct Ser	ata Ile ctc Leu	Ile aaa Lys agt	Leu att Ile 25 tct Ser	Ala 10 cta Leu cca	Gly gaa Glu aag Lys	Leu ata Ile gga	Ile ctg Leu	agg Arg 30	Leu 15 agg Arg	Leu cta Leu tgc	
atg tct gg Met Ser Gi 1 gta agc tt Val Ser Pl gat tgg tg Asp Trp Ti	t ttc ne Phe 20 gg tgg pp Trp	Phe 5 ttg Leu att Ile act	Gly ttg Leu tct Ser	Gly ata Ile ctc Leu gcc	aaa Lys agt Ser 40	Leu att Ile 25 tct Ser atc	Ala 10 cta Leu cca Pro	Gly gaa Glu aag Lys cca	Leu ata Ile gga Gly cat	ctg Leu aaa Lys 45	agg Arg 30 atg Met	Leu 15 agg Arg caa Gln	Leu cta Leu tgc Cys	96
atg tct gg Met Ser Gi  gta agc tg Val Ser Pl  gat tgg tg Asp Trp Ti  gct ttc ca Ala Phe Gi	t ttc he Phe 20 gg tgg rp Trp haa gat hn Asp	Phe 5 ttg Leu att Ile act Thr	Cly ttg Leu tct Ser gga Gly cca	ata Ile ctc Leu gcc Ala 55	aaa Lys agt Ser 40 caa Gln	Leu att Ile 25 tct Ser atc Ile ctt	Ala 10 cta Leu cca Pro tct Ser	Gly gaa Glu aag Lys cca Pro	Leu ata Ile gga Gly cat His 60 tat	ctg Leu aaa Lys 45 tac Tyr	Gly agg Arg 30 atg Met gta Val	Leu 15 agg Arg caa Gln gga Gly	Leu cta Leu tgc Cys tct Ser	96 144
atg tct gg Met Ser Gi  gta agc tt Val Ser Pl  gat tgg tc Asp Trp Ti  3: gct ttc ca Ala Phe Gi 50  tgc ccg tc Cys Pro Ti	t ttc te Phe 20 gg tgg pg Trp aa gat an Asp gg gga pg Gly	Phe 5 ttg Leu att Ile act Thr tgc Cys tta	Ca Pro atc	ata Ile ctc Leu gcc Ala 55 gga Gly	aaa Lys agt Ser 40 caa Gln ttt Phe	Leu att Ile 25 tct Ser atc Ile ctt Leu gta	Ala 10 cta Leu cca Pro tct Ser tgg Trp gca	Gly gaa Glu aag Lys cca Pro acc Thr 75 gca	Leu ata Ile gga Gly cat His 60 tat Tyr	ctg Leu aaa Lys 45 tac Tyr ctc Leu	agg Arg 30 atg Met gta Val agg Arg	Leu 15 agg Arg caa Gln gga Gly ctt Leu	Leu cta Leu tgc Cys tct Ser ttt Phe 80 ctg	96 144 192

Thr Asp Asn	Gly Ser	Thr	Ile L		Gly 105	Lys	Leu	Gln	Trp	Ala 110	Ser	Val	
tca gcc ctt Ser Ala Leu 115			Ile S										384
tct ctc gtc Ser Leu Val													432
tcc tct gcc Ser Ser Ala 145													480
tct gct ctt Ser Ala Leu		Lys											501
<210> 13													
<211> 167		•											
<212> PRT													
<213> duck										٠			
<400> 13													
<400> 13 Met Ser Gly 1	Thr Phe 5	e Gly	Gly I	Ile :	Leu	Ala 10	Gly	Leu	Ile	Gly	Leu 15	Leu	
Met Ser Gly	5			Lys		10					15		
Met Ser Gly 1	5 Phe Let 20	ı Leu	Ile I	Lys	Ile 25	10 Leu	Glu	Ile	Leu	Arg 30	15 Arg	Leu	
Met Ser Gly  1  Val Ser Phe  Asp Trp Trp	Phe Lev 20 Trp Ile	Leu Ser	Ile I	Lys Ser 40	Ile 25 Ser	10 Leu Pro	Glu Lys	Ile Gly	Leu Lys 45	Arg 30 Met	15 Arg Gln	Leu Cys	
Met Ser Gly  1  Val Ser Phe  Asp Trp Trp 35  Ala Phe Gln	Phe Let 20 Trp Ile	Leu Ser	Ile I Leu S A Ala G	Lys Ser 40	Ile 25 Ser Ile	10 Leu Pro Ser	Glu Lys Pro	Ile Gly His 60	Leu Lys 45 Tyr	Arg 30 Met Val	15 Arg Gln Gly	Leu Cys Ser	
Met Ser Gly  Val Ser Phe  Asp Trp Trp 35  Ala Phe Gln 50  Cys Pro Trp	Phe Level 20 Trp Ile Asp The	Leu Ser Gly Fro 70	Ile I Leu S Ala G 55	Lys Ser 40 Gln Phe	Ile 25 Ser Ile Leu	10 Leu Pro Ser	Glu Lys Pro Thr 75	Ile Gly His 60	Leu Lys 45 Tyr	Arg 30 Met Val	Arg Gln Gly Leu	Leu Cys Ser Phe 80	

- 14 -

Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro Lys

Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr Ser

130 Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Leu Thr Gln Leu Ala Thr Leu

145 Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr Leu

160

Ser Ala Leu Phe Tyr Lys Ser 165